



GP1645
Jhu

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

<i>In re</i> Application of)	
)	Group Art Unit: 1645
ZHELNIN and BLOOMQUIST)	
)	Examiner: S. Gucker
Serial No. 09/899,532)	
)	
Filing Date: July 6, 2001)	Docket No. 02973.00040

For: **HUMAN NEUROPEPTIDE Y-LIKE G PROTEIN-COUPLED RECEPTOR**

SUBMISSION OF SUBSTITUTE DECLARATION UNDER 37 C.F.R. § 1.131

U.S. Patent and Trademark Office
220 20th Street S.
Customer Window, Mail Stop Amendment
Crystal Plaza Two, Lobby, Room 1B03
Arlington, VA 22202

Dear Sir:

Applicants responded on June 25, 2004 to the Office Action mailed February 25, 2004 in the application referenced above. The response included a declaration of the inventors under 37 C.F.R. § 1.131, which included Exhibits 1-10. The declaration stated that the dates on Exhibits 1-10 had been redacted; however, the Exhibits 1-10 filed together with the declaration inadvertently contained dates.

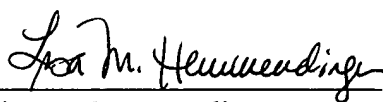
A substitute declaration with Exhibits 1-10 accompanies this paper. The declaration itself is a copy of the one filed June 25, 2004. Exhibits 1-10 are identical to those filed June 25, 2004 except that the dates have been redacted.

Please substitute the declaration and exhibits that accompany this paper for those filed June 25, 2004. Please discard the declaration and exhibits filed June 25, 2004 and delete all copies of the declaration and exhibits that may have been scanned electronically.

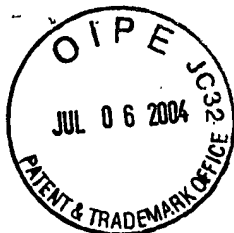
We believe no fee is associated with this request. If a fee is required, please charge our Deposit Account No. 19-0733.

Respectfully submitted,
BANNER & WITCOFF, LTD.

Date: July 6, 2004

By: 
Lisa M. Hemmendinger
Registration No. 42,653

Customer No. 22907



PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:

ZHELNIN and BLOOMQUIST

Serial No. 09/899,532

Filing Date: July 6, 2001

Group Art Unit: 1645

Examiner: S. Gucker

Docket No. 02973.00040

For: HUMAN NEUROPEPTIDE Y-LIKE G PROTEIN-COUPLED RECEPTOR

DECLARATION UNDER 37 C.F.R. § 1.131

U.S. Patent and Trademark Office
220 20th Street S.
Customer Window, Mail Stop Non-Fee Amendment
Crystal Plaza Two, Lobby, Room 1B03
Arlington, VA 22202

Dear Sir:

We, Leonid Zhelnin and Brian Bloomquist, declare as follows:

1. We are the named inventors of the subject matter claimed in the application referenced above.
2. Prior to March 2, 2000, we reduced to practice the subject matter of claims 1-8 and 12 of the application referenced above. The dates on the attached exhibits have been redacted; however, all the work described in this declaration was performed in the United States prior to March 2, 2000.
3. Prior to March 2, 2000, we monitored search results from a program (Gene Agent) that automatically checked sequences released into the public domain for homology to the orexin and NPY1 receptors. Prior to March 2, 2000, we received reports from the orexin-

and NPY1-receptor Gene Agent searches, respectively, indicating that DNAs with accession numbers EM:AC005961 (Homo sapiens Chromosome 11q12.2 PAC pDJ32L16 genomic DNA) and GB:g3823006 (Human sperm genomic library) both had homology to the orexin and NPY1 receptor sequences. Copies of the reports are attached as Exhibit 1. Sequence analysis revealed these DNAs to be overlapping and that AC00596 contained 154,647 nucleotides comprising what appeared to be at least five exons with homology to the orexin receptor. A copy of BLAST comparisons of the translated five exons with the amino acid sequence of the orexin receptor is attached as Exhibit 2.

4. Prior to March 2, 2000, we used sequence information from AC005961 to amplify by polymerase chain reaction (PCR) amplification two PCR products of 234 and 111 bp from genomic DNA. The longer 234 bp clone included both transmembrane domains (TM 1 and 2 of the putative GPCR. A copy of the nucleotide sequence of the PCR product is attached as Exhibit 3.

5. We designed primers to the 5'- and 3'-regions of the 234 bp clone, and 5'- and 3'-RACE amplifications were carried out to clone the full coding region of the putative GPCR. The reverse primers used in the strategy were termed "6A1-85B" and "6A1-126B" and are shown on pages 2 and 3 of Leonid Zhelnin's laboratory notebook no. RB53651. Copies are provided as Exhibit 4.

6. Prior to March 2, 2000, we obtained two 5'-RACE clones (~220 and ~320 bp) from human heart cDNA; sequence analysis of the 5'-RACE clone 5GA1 revealed that it encodes a peptide with homology to the N-terminal 105 amino acids of NPY1. A copy of page 47 of Leonid Zhelnin's laboratory notebook no. RB53651 showing a ClustalW-formatted alignment of the amino acid sequence encoded by 5GA1 and the amino acid sequence of the neuropeptide Y-1

receptor (NPY-1R.pep) is provided as Exhibit 5. The position of the putative START methionine codon (ATG) in clone 5GA1 was consistent with clone 5GA1 being similar to the NPY-1 and orexin-2 receptors. The identity of this ATG as the true START codon was unconfirmed, however, because the open reading frame (ORF) was not closed upstream of the 5'-most ATG.

7. Sequence analysis of the 3'-RACE amplicon (~0.9 kb in length; 3'-RACE #2 clone) revealed that this clone contained sequences homologous to a GPCR through TM6. The primers used in the 3'-RACE strategy were termed "6A1-F32" and "6A1-F41" and are shown on pages 4 and 5 of Leonid Zhelnin's laboratory notebook no. RB53651. Copies are provided as Exhibit 6. However, the 3'-RACE amplicon lacked both a TM7 domain and corresponding STOP codon. A complete clone was electronically assembled from the 3'-RACE amplicon and clone 5GA1 to create a 1047-bp sequence contig, which encoded 349 amino acids and which was named GA1. A copy of page 53 of Leonid Zhelnin's laboratory notebook no. RB53651 showing the electronically assembled sequence is provided as Exhibit 7.

8. Prior to March 2, 2000, GA1 was used as template to search the Image Consortium database for novel expressed sequence tags (ESTs, which are cDNAs) with identity to GA1 to identify the missing 3'-end. Three Image clones from human kidney were identified and found to have similarity based on our previous sequence analysis. Identification of the three Image clones was recorded on page 61 of Leonid Zhelnin's laboratory notebook no. RB53651; a copy is provided as Exhibit 8.

9. Sequence analysis of Image clone 2055185 confirmed the putative START methionine because sequence analysis revealed it to contain an in-frame STOP codon upstream

of the putative START methionine. This sequence information is summarized on page 89 of Leonid Zhelnin's laboratory notebook no. RB53651; a copy is provided as Exhibit 9.

10. Under our direction the 3'-ends of the Image cDNAs (from the NCI_CGAP_Kid12 and Soares NFL_T_GBC_S1 libraries) were sequenced. One of the Image clones had an extended 3'-end that included the presence of a 710-bp intron followed by what appeared to be further exonic sequence.

11. The sequence immediately downstream of the intron of this Image cDNA clone was used as the query to search (via the BLAST algorithm) the genomic sequence within AC005961 to identify the missing 3'-coding region. Prior to March 2, 2000, BLAST analysis identified the missing 271 nucleotides of the 3'-end of the coding region of the GPCR. This sequence information is summarized on page 89 of Leonid Zhelnin's laboratory notebook no. RB53651. See Exhibit 9.

12. Prior to March 2, 2000, we amplified clones containing the complete 1293-bp ORF from both human heart and brain cDNA by PCR (using Marathon-Ready cDNA libraries, Clontech) and recorded this information on page 89 of Leonid Zhelnin's laboratory notebook no. RB53651. See Exhibit 9.

13. Also prior to March 2, 2000, the coding sequence of the full-length cDNA clone was confirmed by sequence analysis of a full-length amplicon generated by PCR from human brain cDNA. This sequence was recorded on pages 95-97 of Leonid Zhelnin's laboratory notebook no. RB53651; copies of these pages are provided as Exhibit 10. The coding sequence is contained within SEQ ID NO:1 of our provisional application Serial No. 60/215,523 and within SEQ ID NO:1 of our utility application 09/899,532. This coding sequence encodes the 431 amino acid sequence shown in SEQ ID NO:2 of both the provisional and utility applications.

14. All statements made herein of our own knowledge are true and all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

Dated: June 25, 2004

Brian T. Bloomquist
Brian Bloomquist, Ph.D.

Dated: June 25, 2004

Leonid Zhelnin
Leonid Zhelnin, Ph.D.



Analysis Results

[Main Menu](#)
[Projects](#)
[Query](#)
[Seq. Analysis](#)
[Utilities](#)
[Login / Logout](#)
[Help](#)

Project ID: orexin Project Name: orexin receptor homology search
 Created: Created By: Zhelmin, Leonid
 Modified: Modified By: lt_Account, Admin
 Status: Current User: Zhelmin, Leonid (WRITE)
 Today's Date: Num Seqs: 7

Analysis Data

These results are saved. Use the buttons to change the state of these results.

[Save these Results](#)
[Delete these Results](#)

Description:

Maximum Number of Hits per Hit Class

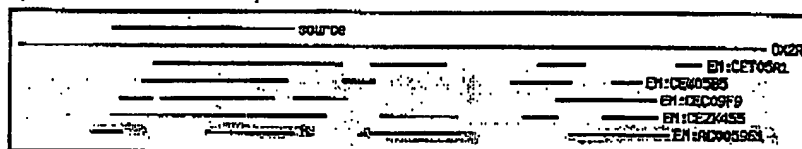
Trans. Protein:

Feature roll-up: ☐ Off ☒ On

[Redisplay](#)

[View parameters](#)

Protein Agent



☐ orexin:OX2R:1

Hit ID	P-Value	% ident.	Description	Hit Class
<input checked="" type="checkbox"/> <u>EM:CEW0585:5</u> Result Details	2.5e-17	40	Caenorhabditis elegans cosmid T05A1	Trans. Protein
	Feature	Description		Feature Metric
	source			Value
		Left End	Right End	Strand
		81	134	+
Hit ID	P-Value	% ident.	Description	Hit Class
<input checked="" type="checkbox"/> <u>EM:CEW0585:5</u> Result Details	4.7e-17	33	Caenorhabditis elegans cosmid W05B5	Trans. Protein
	Feature	Description		Feature Metric
	source			Value
		Left End	Right End	Strand
		74	133	+
Hit ID	P-Value	% ident.	Description	Hit Class
<input checked="" type="checkbox"/> <u>EM:CEW0979:5</u> Result Details	7.4e-17	35	Caenorhabditis elegans cosmid C09F9	Trans. Protein

EM:CEC0979.5 Result Details		source							
		Left End	Right End	Strand	Component Description	Component Metric	Value		
		85	132	+					
Hit ID	P-value	% ident.	Description						Hit Class
EM:CEC0979.5	8.3e-14	26	Caenorhabditis elegans cosmid 2K455						Trans. Protein
Feature		Description					Feature Metric	Value	
source									
		Left End	Right End	Strand	Component Description	Component Metric	Value		
		56	134	+					
Hit ID	P-value	% ident.	Description						Hit Class
EM:ACD03961.1	1.8e-12	32	*** SEQUENCING IN PROGRESS *** Homo sapiens Chromosome 11q12.2 PAC pDJ32L16; HTGS phase 1, 8 unordered pieces.						Trans. Protein
Feature		Description					Feature Metric	Value	
source									
		Left End	Right End	Strand	Component Description	Component Metric	Value		
		112	163	+					

Requested by: Zhelmin, Leonid on

LifeTools
 Biology Software

Project Summary

Main Menu Project Query Seq Analysis Utilities Login / Logout Help

Project ID: orexin Project Name: orexin receptor homology search
 Created: Created By: Zhelmin, Leonid
 Modified: Modified By: It Account, Admin
 Status: Current User: Zhelmin, Leonid (WRITER)
 Today's Date: Num Seqs: 7

Project Members

Project Status

Analysis Tools

Create Agent

Sequences (7 of 7 shown, 7 Active):

Sequence ID	Type	Parent	Created By	Created	Status
<u>orexin:q3823006:1</u>	DNA	GB:q3823006	Zhelmin, L.		OPEN
HS_2052_B1_G04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2052 Col=7 Row=N, genomic survey sequence.					
<u>orexin:AC005961:1</u>	DNA	EM:AC005961	Zhelmin, L.		OPEN
*** SEQUENCING IN PROGRESS *** Homo sapiens Chromosome 11q12.2 PAC pDJ32L16; HTGS phase 1, 8 unordered pieces.					
<u>orexin:frame1 AC005961:1</u>	PRT		Zhelmin, L.		OPEN
<u>orexin:neworex1.pep:1</u>	PRT		Zhelmin, L.		OPEN
<u>orexin:G2897124:1</u>	PRT	ST:G2897124	Zhelmin, L.		OPEN
OREXIN RECEPTOR-1.					
<u>orexin:OX2R:1</u>	PRT		Zhelmin, L.		OPEN
P1:G2897128 - orexin receptor-2 - Homo sapiens (human)					
<u>orexin:AF041243:1</u>	RNA	EM:AF041243	Zhelmin, L.		OPEN
Homo sapiens orexin receptor-1 mRNA, complete cds.					

Manage Sequences

Add Sequences

Gene Agent Results (10 of 166 shown, 166 active):

Agent Name	Results	Started On	Description	Status	Method	Job Status
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed
<u>NEWOREXIN</u>	+			SAVED	Protein Agent	Completed

List All Gene Agent Results

No Project Annotation

List All Annotations


View All Text Annotations

Add New Annotations

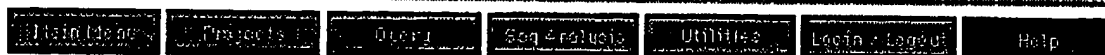
Requested by: Zhelmin, Leonid

LifeTools
biology in silico**Query Detail**[Main Menu](#)[Projects](#)[Query](#)[Seq Analysis](#)[Utilities](#)[Login / Logout](#)[Help](#)Sequence: orexin:AC005961:1 [Add Sequence Annotation](#)

Entries with the same Physical Sequence		FASTA
<u>EM:AC005961</u>		
<u>GB:g3859648</u>		
<u>ImageIga:g3859648:1</u>		
<u>Newgag:AC005961:1</u>		
General Information About The Entry		
Sequence ID	AC005961	
Version	1	
Sequence Description	*** SEQUENCING IN PROGRESS *** Homo sapiens Chromosome 11q12.2 PAC pDJ32L16; HTGS phase unordered pieces. , 8	
Project	orexin	
Project Name	orexin receptor homology search	
Molecule	DNA	
Sequence Information		
Length	154647	

 **INCYTE PHARMACEUTICALS, INC.**

				Small Su
Sequences producing High-scoring Segment Pairs:	Reading Frame	High Score	Proba P(N)	
AC005961 *** SEQUENCING IN PROGRESS *** Homo sapien..	+2	103	1.8e-	
Score = 103 (48.3 bits), Expect = 1.8e-12, Sum P(5) = 1.8e-12				
Identities = 17/52 (32%), Positives = 33/52 (63%), Frame = (+2)				
Query: 112 LVVDITETWFFGQSLCKVIPYLQTVSVSVSVLTLSCIALDRWYAICHPLMFK			163	
L+ D++ G +CK++P++Q+ +V +LT++CIA++R + HP K				
Sbjct: 48452 LMYDLSYFLTAGAFICKKVPFVQSTAVVTEILIMTCIAVERHQGLVHPFKMK			48607	
Score = 88 (41.3 bits), Expect = 1.8e-12, Sum P(5) = 1.8e-12				
Identities = 15/54 (27%), Positives = 31/54 (57%), Frame = (+3)				
Query: 210 CDERWGGEIYPKMYHICFFLVTYMAPLCMLVLAYLQIFRKLWCRQIPGTSSVVQ			263	
C E W ++ K+Y ++ ++ PL +M++ Y +I +LW ++ G SV++				
Sbjct: 56082 CLREWTSPPVHQKIYTTFFILVILFLLPLMVMLILYSKIGYELWIKRVRGDSVLR			56243	
Score = 71 (33.3 bits), Expect = 1.8e-12, Sum P(5) = 1.8e-12				
Identities = 15/54 (27%), Positives = 26/54 (48%), Frame = (+1)				
Query: 329 VFGMFAHTEDRETVYAWFTFSHWLVYANSAANPIIYNFLSGKFRESFKAAPSCC			382	
+ G F D T+ F + ++NS NPI+Y F++ F++ +A C				
Sbjct: 59380 ISGNFEKEYDDVTIKMIFAIVQIIGFSNSICNPVYAFMNENFKKNVLSAVCYC			59541	
Score = 47 (22.1 bits), Expect = 1.8e-12, Sum P(5) = 1.8e-12				
Identities = 9/17 (52%), Positives = 11/17 (64%), Frame = (+2)				
Query: 46 EYLHPKEYEWVLIAGYI			62	
EY H +E W LI+ YI				
Sbjct: 29786 EYPHAEENWTLISQYI			29836	
Score = 46 (21.6 bits), Expect = 1.8e-12, Sum P(5) = 1.8e-12				
Identities = 6/8 (75%), Positives = 7/8 (87%), Frame = (+3)				
Query: 381 CCCLGVHH			388	
CCCLG+ H				
Sbjct: 148295 CCCLGLEH			148319	

**Retrieve
FASTA Sequences**

Project ID: <u>Newpage</u>	Project Name: <u>Cloning new gene agent search sequences</u>
Created:	Created By: <u>Zhelnin, Leonid</u>
Modified:	Modified By: <u>Zhelnin, Leonid</u>
Status: <u>OPEN</u>	Current User: <u>Zhelnin, Leonid (WRITE)</u>
Today's Date:	Num Seqs: <u>30</u>

>Newpage:GA2:1 pcr product of ac ac1 primers of AC00596 genomic chromosome se
GTATGATTATCCTATTTTCCTTACTGCAGGTGCTTTCATTGCAAGATGGTGCCATTGTCCAGTCTACCGCTGTTGTGA
CAGAAATCCTCACTATGACCTGCATTGCTGTGAAAGGCACCAGGGACTTGTGCATCCTTTAAATGAAGTGGCAATAC
ACCAACCGAAGGGCTTTCACAATGCTAGGTGAGCCCACTGGATGTGCCAATGGCAGTGTGAATGACATTCTTCA

Requested by: Zhelnin, Leonid on



BAYER CORPORATION

47

SUBJECT

GA1-5' RACE product

see DNA Sequence 1.3.10

Unlabeled Sequences # 3 - 6 Genes

GA1 sequence 17 bp. 100% identical to 100% identical

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34

5GA1 Aligned Sequences Formatted Alignments

ClustalW Formatted Alignments

5GA1
NPY-1R.pcp

10 20 30
Q A L N I T P E Q F S R L L R D H N L T R E F I L Y R
N S T L F S Q V E N H S V H S N F S E K N A L L F E N

40 50 60
L R P L V Y T P E G R A K L A V T G V L I F A A L
D - - - - D C H L A M I F T A A Y G A V I I G V

70 80 90
F A L V F Y V V T R S A T N F C S A L S
S L A L I I I I L K Q E N L V N S F

100 110 120
I T F F I V M K P
V A I M L F F V Y T L M D H W V F G E A M C K L

SIGNED BY

DATE

WITNESSED AND UNDERSTOOD BY

DATE

DATE _____

BAYER CORPORATION

Touch down PCR for GAT RACE

15	5 μ l cDNA template (Heart) (Brain)	1
10	36 μ l H ₂ O	2
15	5 μ l 10 \times cDNA Buffer	3
3	1 μ l dNTP Mix (10 mM)	4
3	1 μ l Ado cDNA polymer mix (50 \times)	5
	43 μ l Final + 3 μ l AP1	6

Program 1 (preferred: use if GSP $T_m > 70^\circ\text{C}$):

PE DNA Thermal Cycler

PE GeneAmp Systems 2400/9600
(or hot-lid thermal cycler):

• 94°C for 30 sec

• 5 cycles:

94°C 5 sec

72°C 4 min⁰

• 5 cycles:

94°C 5 sec

70°C 4 min⁰

• 20-25 cycles:

94°C 5 sec

68°C 4 min⁰

Heart	1	B126
	2	F32
	3	F41
Brain	4	B126
	5	F32
	6	F41

PRODUCT: Human Heart
Marathon-Ready™ cDNA

CATALOG #: 7404-1

LOT#: 9010719

STORAGE BUFFER:

- 10 mM Tricine-KOH (pH 9.2)
- 1 mM EDTA

STORAGE CONDITIONS:

- -20°C
- Avoid multiple freeze/thaw cycles.

SHELF LIFE:

1 year from date of receipt under proper storage conditions

DESCRIPTION:

Marathon-Ready cDNA is high-quality, double-stranded cDNA which has been ligated to the Marathon™ Adaptor and is ready for use as a template in 5' and 3' Marathon RACE reactions. In many cases, the full-length cDNA can then be obtained by end-to-end amplification or standard cloning. Enough material is provided for 30 50- μ l Marathon RACE reactions.

CONCENTRATION: \approx 0.1 ng/ μ lPOLY A⁺ RNA SOURCE:

Normal, whole hearts pooled from 3 male Caucasians, ages 28-47; cause of death: trauma

No further RNA source information is available.

SIGNED BY

DATE

WITNESSED AND UNDERSTOOD BY

DATE

CROSS REFERENCES

BAYER CORPORATION

61

SUBJECT

mage clones matching 6A1

Im	2055532	g4001837	1
Im	2055185	g4002759	2
Im	2091776	g4187861	3
			4
			5
			6
			7

DNA vs EST Homology Search

source	g4001837
GB:g400 337	
GB:g400 759	
GB:g4187861	

g4001837

Hit ID #	P-Value	% ident.	Description
GB:g4001837 (Detail)	0	100	tb27a03.x1 NCI_CGAP_Kid12 Homo sapiens cDNA
Feature	Start	Stop	Description
source	1	432	

Analysis Results: 28499

http://lifetools-a.wh.bayer.com/cgi-bin/incyte/LifeTools/2.0/LT_viewer?id=28499

Hit ID #	P-Value	% ident.	Description
GB:g4002759 (Detail)	0	100	tb23d09.x1 NCI_CGAP_Kid12 Homo sapiens cDNA
Feature	Start	Stop	Description
source	1	432	

AM

Hit ID #	P-Value	% ident.	Description
GB:g4187861 (Detail)	6.2e-43	100	tc67e05.x1 Soares_NFL_T_GBC_S1 Homo sapiens
Feature	Start	Stop	Description
source	3	127	

Acc. Num.	Image/Unigene TIGR Indices	Insert Length	Read Length	HQSS	Source (Age/Sex)	
AI307658	Im:2055532 Hs.181638	1414	432	419	NCI_CGAP_Kid12 library made from kidney (2 pooled tumors (clear cell type))	20 27 28 29
AI308124	Im:2055185 Hs.181638	1308	432	429	NCI_CGAP_Kid12 library made from kidney (2 pooled tumors (clear cell type))	30 31 32
AI378908	Im:2091776 Hs.181638	404	364		Soares_NFL_T_GBC_S1 library made from pooled	33 34

SIGNED BY

DATE

WITNESSED AND UNDERSTOOD BY

DATE

CROSS REFERENCE

NRX-like clow and primors

DNA sequence 1902 b.p. TGGCCCTCGAGG ... CTGATTCCTTC 11 bases

[illegible]

DATE: _____

DATE _____

CROSS REFERENCES:

BAYER CORPORATION

Sequencing results of LG21/pTZBlue

1. Check if I. Taylor going to done P.E. receptor

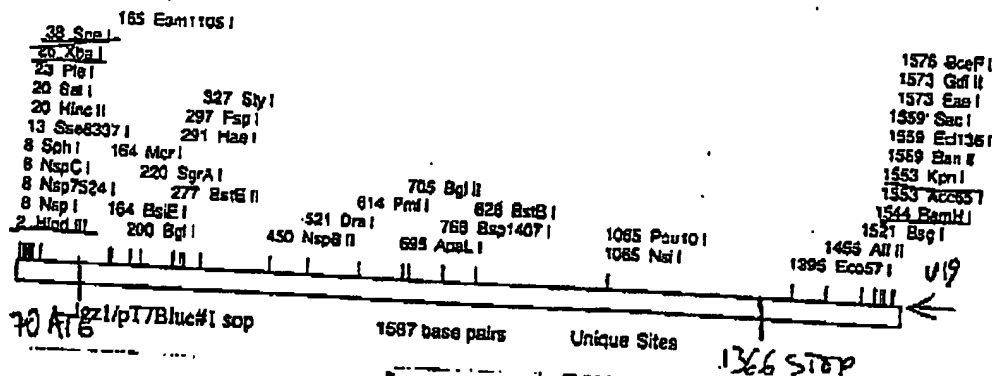
1). Clone #1 sop is ok with one polymorphism

DNA Strider™ 1.2

lgz1/pT7Blac#1 sop -> Graphic Map

DNA sequence 1387 b.p. ~~caagcagcagc ... ccgtccgtttac~~ linear

432 AA



2) Clone # 7 H. Brain is good (same orientation with ttt \rightarrow ttt (Phe) 917 AA

3) clone #16 H. marit is good
with: atc \rightarrow Att (16) 216 AA

↓ cloned using TA- κ T
in penta 310 His.

X^R 6a / Sam 3.1.1 -
April (L)

SIGNED BY

BAYER CORPORATION

SUBJECT

Full length cDNA of LGZ1 (npv-like)

$\mu_{DNA} = 3.1 \times 10^{-20}$

#1scop/pcDNA3.1Topo
Sequencer™ "Untitled Project"

HindIII (6)
KpnI (16)
SacI (22)
BamHI (24)
SpeI (30)
BstXI (43)
SmaI (61)

PstI (1560)
EcoRV (1563)
BstXI (1573)
NotI (1578)
XmaIII (1578)
XhoI (1584)
XbaI (1590)
DraII (1596)
ApaI (1600)
SacII (1603)

PstI (1113) EcoRI (1344)

ATG (69)

Mapping all cutsites.

Mapping all cutsites.
Cutters : ApaI, BamHI, BstXI, DraII, EcoRI, EcoRV, HindIII, KpnI, NotI, PstI, SacI, SacII, SmaI, SpeI, XbaI, XhoI & XmaII
Non-Cutters : Bsp106 & SalI

start

STANDARD, 1950
SPECIAL, 1950

WITNESSED AND UNDERSTOOD BY

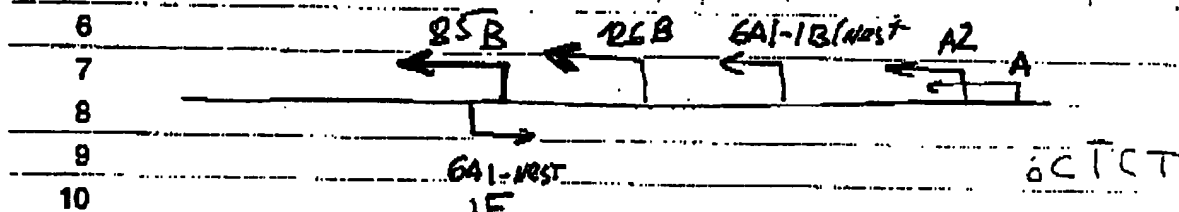
CROSS REFERENCES:

BAYER CORPORATION

SUBJECT

5' RACE 641

1	9	1	85	85	54.1	74.1	4.9	54.1	56.8	61.7	48.1	60.9	-3.3	-7.9			
2			CCATCTAATACGACTCTATAGCC 27 -43.1 -205.0 -536.4										GGTCATACGATGACATGAC 25 -41.9 -184.5 -470.9				6A1-8
3	10	1	126	126	54.8	77.0	1.7	56.0	56.8	59.6	48.1	49.0	-1.3	-7.8			
4			CCATCTAATACGACTCTATAGCC 27 -43.1 -205.0 -536.4										GGTCATACGATGACATGAC 25 -40.2 -182.9 -471.0				6A1-



GA1.txt Translated Sequence

Sequence Range: 1 to 161

Range: 1 to 161
Double strand probe

6A1-85B 6A1-FY1

10 20 30 40 50
 CACCTCGTGT ACCAG AGTGTA CTCTTTGGCAATGCTCTGGTGTCTACGT
 TCACATGAGTAGCGGGACCGGAGAAACCGTTACGAGACCAAGATGCA
 S V L I A L A L P G N A L V E Y V

probe

TRANSLATION OF GA1.TXT [A]

641-126B

60 70 80 90 100
GGTGACCCGCGAGCAAGGCCATGCGGCACCGTCACCAACATCTTTATCTGCT
CCACTGGGCGTCGTTCCGGTACCGGTGGCAGTCGTTGTAGAANTAGACGA
V T R S K A M R T V T N I F I C>

TRANSLATION OF GAL.TXT [A]

6A1-1B 6A1-BA2

6A1-BA (Angrä)

116 120 130 140 150
CCTGGGCGCTCAGTGACCTGCTATCACCTCTCTTCGATTCCCGTCACC
CGAACCGGCACTCTCTGACCGAGTAGTGGAGGACGTAATGCGAGTGG
S L A H S U S F C I P V T>
TRANSLATION OF GA1.TXT [A]

TRANSLATION OF GA1.TXT [A]

160
ATGAAGCCGAA
TACTTCGGCTT
M A P X

5 primers for 5' RACE

probe:

SIGNED BY_

WITNESSED AND UNDERSTOOD BY

DATE

CROSS REFERENCES:

3

CROSS REFERENCES: